



## SEQUENCE LISTING

<110> Yanofsky, Martin F.  
The Regents of the University of California

<120> Methods of Suppressing Flowering in Transgenic Plants

<130> 19452A-002210US

<140> US 09/869,582

<141> 2002-02-28

<150> US 60/104,604

<151> 1998-10-16

<150> WO PCT/US99/24407

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<170> PatentIn Ver. 2.1

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 <223> AGL2 cDNA

<220>  
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 aataacccta taaataaaaa atcagacaaa cagaagttt ctttttttccatatacc tcaattctcc 180  
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 agaccataaa aactcaaaaa gatcagatct ttccctctgaa aaagagatac ccaacttatg 300  
 tttttgtgtg tctgtatata gataaacatt acatacccat atttgtgtat agacataaaa 360  
 agtggaaatt aaggtaacaa aaagaa atg gga aga gga aga gta gag ctg aag 413  
 Met Gly Arg Gly Arg Val Glu Leu Lys  
 1 5

agg ata gag aac aaa atc aac aga caa gta acg ttt gca aag cgt agg 461  
 Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe Ala Lys Arg Arg  
 10 15 20 25

aac ggt ttg ttg aag aaa gct tat gaa ttg tct gtt ctc tgt gat gct 509  
 Asn Gly Leu Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu Cys Asp Ala  
 30 35 40

gaa gtt gct ctc atc atc ttc tcc aac cgt gga aag ctc tat gag ttt	557
Glu Val Ala Leu Ile Ile Phe Ser Asn Arg Gly Lys Leu Tyr Glu Phe	
45 50 55	
tgc agc tcc tca aac atg ctc aag aca ctt gat cgg tac cag aaa tgc	605
Cys Ser Ser Ser Asn Met Leu Lys Thr Leu Asp Arg Tyr Gln Lys Cys	
60 65 70	
agc tat gga tcc att gaa gtc aac aac aaa cct gcc aaa gaa ctt gag	653
Ser Tyr Gly Ser Ile Glu Val Asn Asn Lys Pro Ala Lys Glu Leu Glu	
75 80 85	
aac agc tac aga gaa tat ctg aag ctt aag ggt aga tat gag aac ctt	701
Asn Ser Tyr Arg Glu Tyr Leu Lys Leu Lys Gly Arg Tyr Glu Asn Leu	
90 95 100 105	
caa cgt caa cag aga aat ctt ctt ggg gag gat tta gga cct ttg aat	749
Gln Arg Gln Gln Arg Asn Leu Leu Gly Glu Asp Leu Gly Pro Leu Asn	
110 115 120	
tca aag gag tta gag cag ctt gag cgt caa ctg gac ggc tct ctc aag	797
Ser Lys Glu Leu Glu Gln Leu Glu Arg Gln Leu Asp Gly Ser Leu Lys	
125 130 135	
caa gtt cgg tcc atc aag aca cag tac atg ctt gac cag ctc tcg gat	845
Gln Val Arg Ser Ile Lys Thr Gln Tyr Met Leu Asp Gln Leu Ser Asp	
140 145 150	
ctt caa aat aaa gag caa atg ttg ctt gaa acc aat aga gct ttg gca	893
Leu Gln Asn Lys Glu Gln Met Leu Leu Glu Thr Asn Arg Ala Leu Ala	
155 160 165	
atg aag ctg gat gat atg att ggt gtg aga agt cat cat atg gga gga	941
Met Lys Leu Asp Asp Met Ile Gly Val Arg Ser His His Met Gly Gly	
170 175 180 185	
tgg gaa ggc ggt gaa cag aat gtt acc tac gcg cat cat caa gct cag	989
Trp Glu Gly Glu Gln Asn Val Thr Tyr Ala His His Gln Ala Gln	
190 195 200	
tct cag gga cta tac cag cct ctt gaa tgc aat cca act ctg caa atg	1037
Ser Gln Gly Leu Tyr Gln Pro Leu Glu Cys Asn Pro Thr Leu Gln Met	
205 210 215	
ggg tat gat aat cca gta tgc tct gag caa atc act gcg aca aca caa	1085
Gly Tyr Asp Asn Pro Val Cys Ser Glu Gln Ile Thr Ala Thr Thr Gln	
220 225 230	
gct cag gcg cag ccg gga aac ggt tac att cca gga tgg atg ctc tga	1133
Ala Gln Ala Gln Pro Gly Asn Gly Tyr Ile Pro Gly Trp Met Leu	
235 240 245	
gaatcatgta ctgtgatgaa gctcacccac aaaagacctt atatatatat aaagtataga	1193
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   20                 25                         30  
 Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ala Leu Ile Ile Phe  
   35                 40                         45  
 Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Ser Ser Asn Met Leu  
   50                 55                         60  
 Lys Thr Leu Asp Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val  
   65                 70                         75                         80  
 Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu  
   85                 90                         95  
 Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu  
   100                 105                     110  
 Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu  
   115                 120                     125  
 Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Ser Ile Lys Thr  
   130                 135                     140  
 Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Asn Lys Glu Gln Met  
   145                 150                     155                     160  
 Leu Leu Glu Thr Asn Arg Ala Leu Ala Met Lys Leu Asp Asp Met Ile  
   165                 170                     175  
 Gly Val Arg Ser His His Met Gly Gly Trp Glu Gly Gly Glu Gln Asn  
   180                 185                     190  
 Val Thr Tyr Ala His His Gln Ala Gln Ser Gln Gly Leu Tyr Gln Pro  
   195                 200                     205  
 Leu Glu Cys Asn Pro Thr Leu Gln Met Gly Tyr Asp Asn Pro Val Cys  
   210                 215                     220  
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   225                 230                     235                     240  
 Gly Tyr Ile Pro Gly Trp Met Leu  
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<220>  
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 taattaaagt tttctctcta gctattcctc ttctttctt gttcttgaaa actagggttt 180

acttcaccaa aagataagat ctttccccag aaaaagcaat acccaagtca tgtttctgtg 240  
 tgtctgtata tagataaaac attacataacc ctaataaggt tacacaaata gctataaaag 300  
 agggaaaata agatagggat tttttggggt gaggaaag atg gga aga gga aga gta 356  
 Met Gly Arg Gly Arg Val  
 1 5  
 gag ctc aag agg ata gag aac aaa atc aac aga caa gtg acg ttt gct 404  
 Glu Leu Lys Arg Ile Glu Asn Lys Ile Asn Arg Gln Val Thr Phe Ala  
 10 15 20  
 aaa cgt aga aat ggt ttg ctg aaa aaa gct tat gag ctt tct gtt ctc 452  
 Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala Tyr Glu Leu Ser Val Leu  
 25 30 35  
 tgc gat gct gaa gtc tct ctc atc gtc ttc tcc aac cgt ggc aag ctc 500  
 Cys Asp Ala Glu Val Ser Leu Ile Val Phe Ser Asn Arg Gly Lys Leu  
 40 45 50  
 tac gag ttc tgc agc acc tcc aac atg ctc aag aca ctg gaa agg tat 548  
 Tyr Glu Phe Cys Ser Thr Ser Asn Met Leu Lys Thr Leu Glu Arg Tyr  
 55 60 65 70  
 cag aag tgt agc tat ggc tcc att gaa gtc aac aac aaa cct gct aaa 596  
 Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val Asn Asn Lys Pro Ala Lys  
 75 80 85  
 gag ctt gag aac agc tac aga gag tac ttg aag ctg aaa ggt aga tat 644  
 Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu Lys Leu Lys Gly Arg Tyr  
 90 95 100  
 gaa aat ctg caa cgt cag cag aga aat ctt ctt gga gag gat ctt gga 692  
 Glu Asn Leu Gln Arg Gln Arg Asn Leu Leu Gly Glu Asp Leu Gly  
 105 110 115  
 cct ctg aat tca aag gag cta gag cag ctt gag cgt caa cta gac ggc 740  
 Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu Glu Arg Gln Leu Asp Gly  
 120 125 130  
 tct ctg aag caa gtt cgc tgc atc aag aca cag tat atg ctt gac cag 788  
 Ser Leu Lys Gln Val Arg Cys Ile Lys Thr Gln Tyr Met Leu Asp Gln  
 135 140 145 150  
 ctc tct gat ctt caa ggt aag gag cat atc ttg ctt gat gcc aac aga 836  
 Leu Ser Asp Leu Gln Gly Lys Glu His Ile Leu Leu Asp Ala Asn Arg  
 155 160 165  
 gct ttg tca atg aag ctg gaa gat atg atc ggc gtt aga cat cac cat 884  
 Ala Leu Ser Met Lys Leu Glu Asp Met Ile Gly Val Arg His His His  
 170 175 180  
 ata gga gga gga tgg gaa ggt ggt gat caa cag aat att gcc tat gga 932  
 Ile Gly Gly Gly Trp Glu Gly Asp Gln Gln Asn Ile Ala Tyr Gly  
 185 190 195  
 cat cct cag gct cat tct cag gga cta tac caa tct ctt gaa tgt gat 980  
 His Pro Gln Ala His Ser Gln Gly Leu Tyr Gln Ser Leu Glu Cys Asp  
 200 205 210

ccc act ttg caa att gga tat agc cat cca gtg tgc tca gag caa atg	215	220	225	230	1028
Pro Thr Leu Gln Ile Gly Tyr Ser His Pro Val Cys Ser Glu Gln Met					
gct gtg acg gtg caa ggt cag tcc caa caa gga aac ggc tac atc cct	235	240	245		1076
Ala Val Thr Val Gln Gly Gln Ser Gln Gln Gly Asn Gly Tyr Ile Pro					
ggc tgg atg ctg tga gcgatacttc ttccccaaat aaagatctta agcaagtact	250				1131
Gly Trp Met Leu					
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aagacttttg ctttttaga cacaagtggc tatagctgta atagccttca acatctctct					1251
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Tyr Glu Leu Ser Val Leu Cys Asp Ala Glu Val Ser Leu Ile Val Phe	35	40	45		
Ser Asn Arg Gly Lys Leu Tyr Glu Phe Cys Ser Thr Ser Asn Met Leu	50	55	60		
Lys Thr Leu Glu Arg Tyr Gln Lys Cys Ser Tyr Gly Ser Ile Glu Val	65	70	75	80	
Asn Asn Lys Pro Ala Lys Glu Leu Glu Asn Ser Tyr Arg Glu Tyr Leu	85	90	95		
Lys Leu Lys Gly Arg Tyr Glu Asn Leu Gln Arg Gln Gln Arg Asn Leu	100	105	110		
Leu Gly Glu Asp Leu Gly Pro Leu Asn Ser Lys Glu Leu Glu Gln Leu	115	120	125		
Glu Arg Gln Leu Asp Gly Ser Leu Lys Gln Val Arg Cys Ile Lys Thr	130	135	140		
Gln Tyr Met Leu Asp Gln Leu Ser Asp Leu Gln Gly Lys Glu His Ile	145	150	155	160	
Leu Leu Asp Ala Asn Arg Ala Leu Ser Met Lys Leu Glu Asp Met Ile	165	170	175		
Gly Val Arg His His Ile Gly Gly Trp Glu Gly Gly Asp Gln	180	185	190		
Gln Asn Ile Ala Tyr Gly His Pro Gln Ala His Ser Gln Gly Leu Tyr	195	200	205		
Gln Ser Leu Glu Cys Asp Pro Thr Leu Gln Ile Gly Tyr Ser His Pro	210	215	220		

Val	Cys	Ser	Glu	Gln	Met	Ala	Val	Thr	Val	Gln	Gly	Gln	Ser	Gln	Gln
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Gly	Asn	Gly	Tyr	Ile	Pro	Gly	Trp	Met	Leu						
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<220>  
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Ser Met Leu Arg Thr Leu Glu Arg Tyr Gln Lys Cys Asn Tyr Gly Ala  
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cag cag gag tat ctc aag ctt aag gag cgt tat gac gcc tta cag aga 339  
Gln Gln Glu Tyr Leu Lys Leu Lys Glu Arg Tyr Asp Ala Leu Gln Arg  
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acc caa agg aat ctg ttg gga gaa gat ctt gga cct cta agt aca aag 387  
Thr Gln Arg Asn Leu Leu Gly Glu Asp Leu Gly Pro Leu Ser Thr Lys  
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gag ctt gag tca ctt gag aga cag ctt gat tct tcc ttg aag cag atc 435  
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aga gct ctc agg aca cag ttt atg ctt gac cag ctc aac gat ctt cag 483  
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 His Asn Met Pro Pro Pro Leu Pro Pro Gln Gln His Gln Ile Gln His  
 195 200 205  
 Pro Tyr Met Leu Ser His Gln Pro Ser Pro Phe Leu Asn Met Gly Gly  
 210 215 220  
 Leu Tyr Gln Glu Asp Asp Pro Met Ala Met Arg Arg Asn Asp Leu Glu  
 225 230 235 240  
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 aagaaaagcta attaaagttt tctctctagc tattccttctt cttttcttctgt tcttgaaaac 180  
 tagggtttac ttcacccaaaa gataagatct ttccccagaa aaagcaatac ccaagtcatg 240  
 tttctgtgtg tctgtatata gataaaaacat tacataccct aataaggta cacaatagc 300  
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 aaatggtttgc tggaaaaaaag cttatgagct ttctgttctc tgcgatgctg aagtctct 480  
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 gtgctcagag caaatggctg tgacggtgca aggtcagtcc caacaaggaa acggctacat 1080  
 ccctggctgg atgctgtgag cgatacttct tcccccaata aagatcttaa gcaagtactg 1140  
 gtgggggtctt cgtgggtgta tcttagatct tatgcatatg aataataatg ttattgcaca 1200  
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 ctgtttcagg atttgggttgc gcctattgtt attgcttata tatgtatggt ttgtataatg 1320  
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 aaaagaatca ataaccctat aaataaaaaaa tcagacaaac agaagttcc tcttcttctt 180  
 ccttaagcta gtacccttttgc ttcttgcatt tagggtaat ttctttttc caaataccat 240  
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 agaggataga gaacaaaatc aacagacaag taacgttgc aaagcgttagg aacgggtttgt 480  
 tgaagaaagc ttatgaattt tctgttctt gtatgtctt agttgtctc atcatcttctt 540  
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 gagaatcatg tactgtgtt gaaatgttgc acaaaaagacc ttatataatata ataaatgtt 1200  
 gatataagac ttggatttttgc agacataatgtt ggcgttgc tggatgtttttt 1260  
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30

<210> 18  
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<220>  
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28